AMENDMENTS

In the specification:

 Please replace the paragraph beginning on line page 47, line 5 with the following rewritten paragraph:

 The alignment of GFP-like proteins (see supplemental data) was constructed after Matz, M. V., Fradkov, A. F., Labas, Y. A., Savitsky, A. P., Zaraisky, A. G., Markelov, M. L. & Lukyanov, S. A. (1999) *Nat Biotechnol* 17, 969-73 taking in account constraints of the protein structure. Then the DNA alignment was made following the protein alignment; excluding the poorly aligned N- and C-terminal regions. The phylogenetic tree was constructed using Tree-Puzzle software (Strimmer, K. & von Haeseler, A. (1996) *Mol. Biol. Evol.* 13, 964-969) under HKY model of DNA evolution (Hasegawa, M., Kishino, H. & Yano, K. (1985) *J. Mol. Evol.* 22, 160-174), assuming that the variability of sites follows gamma-distribution with alpha parameter estimated from the dataset. The tree was confirmed to be the maximum likelihood tree by PAML software (Yang, Z. (2000) (University College (**available on the worldwide web at** http://abacus.gene.ucl.ac.uk/software/paml.html), London, England)) under REV model (Yang, Z. H., Goldman, N. & Friday, A. (1994) *Molecular Biology and Evolution* 11, 316-324). The tree built by Tree-Puzzle from protein alignment (JTT model, (Jones, D. T., Taylor, W. R. & Thornton, J. M. (1992) *CABIOS* 8, 275-282) had the same topology but lower support values due to smaller number of informative sites in the protein alignment.